

Qy 1 MKKRTLSLFGMLLIGLLESGSLPYPNPAEAASSASAVKGDVYQIILIDFYDGDITNN 60
 1 MKKRTLSLFGMLLIGLLESGSLPYPNPAEAASSASAVKGDVYQIILIDFYDGDITNN 60

Db 61 NPAKSGLYDPTKSKWKMVWQGDLEGVRQKPYLKQGVTTIWLSVLNDLTDLAGTDTN 120
 61 NPAKSGLYDPTKSKWKMVWQGDLEGVRQKPYLKQGVTTIWLSVLNDLTDLAGTDTN 120

Qy 121 GHGKWTDFPKQIEHFGNWTFDTLVNDAHQNGIKVIVDFPVNHSPTFKANDSTAEGG 180
 121 GHGKWTDFPKQIEHFGNWTFDTLVNDAHQNGIKVIVDFPVNHSPTFKANDSTAEGG 180

Qy 181 ALYNGTYMNYFDDATKGYFHNGD1ISWDDRYTAQWNKNTDPAGFSLADLSQENGTIA 240
 181 ALYNGTYMNYFDDATKGYFHNGD1ISWDDRYTAQWNKNTDPAGFSLADLSQENGTIA 240

Qy 241 QYLTDAYOLVVAHAGDLGLRDAVKHFNFSFSKSLADKLYQKKDIFLVGENYQDDPGTANH 300
 241 QYLTDAYOLVVAHAGDLGLRDAVKHFNFSFSKSLADKLYQKKDIFLVGENYQDDPGTANH 300

Db 301 LEKYRANNSGVNVLDFTDINTVNTENVGCFPTOTMDLNMMVNQTGNEYKVKENLTFFIDN 360
 301 LEKYRANNSGVNVLDFTDINTVNTENVGCFPTOTMDLNMMVNQTGNEYKVKENLTFFIDN 360

Db 298 LEKYRANNSGVNVLDFTDINTVNRVGFTFTQMDLNMMVNQTGNEYKVKENLTFFIDN 357
 298 LEKYRANNSGVNVLDFTDINTVNRVGFTFTQMDLNMMVNQTGNEYKVKENLTFFIDN 357

Qy 361 HDMSRFELSYNS-NKANLHQ-ALAFILTSRG-TSIVYGTDEQYMAAGDNDYNGRAMPADFT 417
 361 HDMSRFELSYNS-NKANLHQ-ALAFILTSRG-TSIVYGTDEQYMAAGDNDYNGRAMPADFT 417

Db 358 HDMSRFELSYNSNKANLHQRLSFL--RGVRPRPIYYGTEQYMAAGDNDYNGRAMPADFT 415
 358 HDMSRFELSYNSNKANLHQRLSFL--RGVRPRPIYYGTEQYMAAGDNDYNGRAMPADFT 415

Qy 418 TTAFKVESTLAGLRNRRNAIAQGTTORWINNDVYITERKFENDVVLVAINRNTQSSVS 477
 418 TTAFKVESTLAGLRNRRNAIAQGTTQRWINNDVYITERKFENDVVLVAINRNTQSSVS 477

Db 416 TTAFKVESTLAGLRNRRNAIAQGTTQRWINNDVYITERKFENDVVLVAINRNTQSSVS 475
 416 TTAFKVESTLAGLRNRRNAIAQGTTQRWINNDVYITERKFENDVVLVAINRNTQSSVS 475

Qy 478 ISGLQTALPNGSADYSLGLLGNGISVNGSYASFTLAPGAVSVWQSTSASAPOQSY 537
 478 ISGLQTALPNGSADYSLGLLGNGISVNGSYASFTLAPGAVSVWQSTSASAPOQSY 537

Db 476 ISGLQTALPNGSADYSLGLLGNGISVNGSYASFTLAPGAVSVWQSTSASAPOQSY 535
 476 ISGLQTALPNGSADYSLGLLGNGISVNGSYASFTLAPGAVSVWQSTSASAPOQSY 535

Qy 538 APNMGIQGNVVTIDKGKFGTTGTVFQGTVATKSYTSNRLIEVYVPMNAAGLTDVYKTA 597
 538 APNMGIQGNVVTIDKGKFGTTGTVFQGTVATKSYTSNRLIEVYVPMNAAGLTDVYKTA 597

Db 536 APNMGIQGNVVTIDKGKFGTTGTVFQGTVATKSYTSNRLIEVYVPMNAAGLTDVYKTA 595
 536 APNMGIQGNVVTIDKGKFGTTGTVFQGTVATKSYTSNRLIEVYVPMNAAGLTDVYKTA 595

Qy 598 GGVSNNSYNLSGTSQVTFVKSAPPTNGDKVILTGNTPELGWSTDISGAVNNAQ 657
 598 GGVSNNSYNLSGTSQVTFVKSAPPTNGDKVILTGNTPELGWSTDISGAVNNAQ 657

Db 596 GGVSNNSYNLSGTSQVTFVKSAPPTNGDKVILTGNTPELGWSTDISGAVNNAQ 655
 596 GGVSNNSYNLSGTSQVTFVKSAPPTNGDKVILTGNTPELGWSTDISGAVNNAQ 655

Qy 658 GPLLAQNPDWYEVSPVAGKTIQKFIFKRADGTIOWENGNSNHVATPTGATGNITVW 717
 658 GPLLAQNPDWYEVSPVAGKTIQKFIFKRADGTIOWENGNSNHVATPTGATGNITVW 717

Db 656 GPLLAQNPDWYEVSPVAGKTIQKFIFKRADGTIOWENGNSNHVATPTGATGNITVW 715
 656 GPLLAQNPDWYEVSPVAGKTIQKFIFKRADGTIOWENGNSNHVATPTGATGNITVW 715

Qy 718 QN 719
 716 QN 717

Db 716 QN 717

RESULT 2
 CDGT_BACCI
 ID CDT_BACCI
 STANDARD; PRT; 718 AA.
 AC P30920;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DE Cyclomaltoextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin glycosyltransferase) (CGTase).
 OS Bacillus circulans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1397;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=8;
 RX MEDLINE=1103970; PubMed=1368573;
 RA Nitschke L.; Heeger K.; Bender H.; Schulz G. E.;
 RT "Molecular cloning, nucleotide sequence and expression in Escherichia
 coli of the beta-cyclodextrin glycosyltransferase gene from Bacillus
 circulans strain no. 8.";
 DR ProDom; PD001568; CBD_4; 1.

App1. Microbiol. Biotechnol. 33:542-546(1990).
 [2] X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RN RP STRAIN=8;
 RC MEDLINE=91171298; PubMed=1826034;
 RA Klei C.; Schulz G. E.;
 RT "Structure of cyclodextrin glycosyltransferase refined at 2.0 A resolution."
 RR RL Mol. Biol. 217:737-750(1991).
 RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
 RX MEDLINE=90064533; PubMed=2531228;
 RA Hofmann B. E.; Bender H.; Schulz G. E.;
 RT "Three-dimensional structure of cyclodextrin glycosyltransferase from Bacillus circulans at 3.4-A resolution.";
 RN [4] J. Mol. Biol. 209:793-800(1989).
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RC MEDLINE=9558324; PubMed=9558626;
 RA Schmid A. K.; Cortaz S.; Driigez H.; Schulz G. E.;
 RT "Structure of cyclodextrin glycosyltransferase complexed with a derivative of its main product beta-cyclodextrin.";
 RT Biochemistry 37:5909-5915(1998).
 RN [5] J. Mol. Biol. 293:101-110(2000).
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RC MEDLINE=98409292; PubMed=9738912;
 RA Parslegla G.; Schmidt A. K.; Schulz G. E.;
 RT "Substrate binding to a cyclodextrin glycosyltransferase and mutations increasing the gamma-cyclodextrin production.";
 RL Eur. J. Biochem. 255:710-714(1998).
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: MONOMER.
 CC -1- SUBUNIT: TWO CALCIUM IONS.
 CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE MALTOOLIGOSACCHARIDE PRODUCED.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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CC -1- DR EMBL; X68326; CAA84011; -
 DR PIR; S23674; ALBSCC.
 DR PDB; 1CGT; 31-JAN-94.
 DR PDB; 1CGT; 31-JAN-94.
 DR PDB; 3CGT; 27-MAY-98.
 DR PDB; 4CGT; 12-AUG-98.
 DR PDB; 5CGT; 12-AUG-98.
 DR PDB; 6CGT; 14-OCT-98.
 DR PDB; 7CGT; 12-AUG-98.
 DR PDB; 8CGT; 14-OCT-98.
 DR PDB; 9CGT; 14-OCT-98.
 DR InterPro; IPR000461; Alpha_amylase.
 DR InterPro; IPR002044; CBD_4.
 DR InterPro; IPR002909; IPT_TIG.
 DR Pfam; PF00128; alpha_amylase; 1.
 DR Pfam; PF00686; CBM_20; 1.
 DR Pfam; PF01833; TIG; 1.
 DR Pfam; PF02806; alpha_amylase_C; 1.
 DR ProDom; PD001568; CBD_4; 1.